

**RAW SEQUENCE LISTING**

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Application Serial Number: 10/576,778  
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Date Processed by STIC: 3/6/07

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IFWO

## RAW SEQUENCE LISTING

DATE: 03/06/2007

PATENT APPLICATION: US/10/576,778

TIME: 11:18:57

Input Set : N:\efs\03\_06\_07\10576778\_efs\Sequence\_Listing.txt

Output Set: N:\CRF4\03062007\J576778.raw

3 <110> APPLICANT: Ruiz Caston, Jose et al.

5 <120> TITLE OF INVENTION: PROCESS FOR PRODUCING IN YEASTS EMPTY VIRAL CAPSIDS  
CONSISTING OF

6 PROTEINS DERIVED FROM PVP2 OF THE INFECTIOUS BURSAL DISEASE

7 VIRUS (IBDV)

9 <130> FILE REFERENCE: 7572-74819

11 <140> CURRENT APPLICATION NUMBER: US 10/576,778

12 <141> CURRENT FILING DATE: 2006-04-21

14 <150> PRIOR APPLICATION NUMBER: PCT/ES2005/070052

15 <151> PRIOR FILING DATE: 2005-04-27

17 <150> PRIOR APPLICATION NUMBER: P200401044

18 <151> PRIOR FILING DATE: 2004-04-30

20 <160> NUMBER OF SEQ ID NOS: 11

22 <170> SOFTWARE: PatentIn version 3.3

24 <210> SEQ ID NO: 1

25 <211> LENGTH: 7929

26 <212> TYPE: DNA

27 <213> ORGANISM: Artificial

29 <220> FEATURE:

30 <223> OTHER INFORMATION: Nucleotide sequence of plasmid pESCURAinv/pVP2-456

33 <220> FEATURE:

34 <221> NAME/KEY: promoter

35 <222> LOCATION: (1)..(342)

36 <223> OTHER INFORMATION: Promotor Gall

38 <220> FEATURE:

39 <221> NAME/KEY: CDS

40 <222> LOCATION: (351)..(1721)

42 <400> SEQUENCE: 1

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47	tgataatgcg attagttttt tagccttatt tctggggtaa ttaatcagcg aagcgatgat	180
49	ttttgatcta ttaacagata tataaatgca aaaactgcat aaccacttta actaatactt	240
51	tcaacatttt cggtttgtat tacttcttat tcaaagttaa taaaagtatc aacaaaaaat	300
53	tgttaatata cctctatact ttaacgtcaa ggagaaaaaa ccccggatct atg aca	356
54		Met Thr
55		1
57	aac ctg tca gat caa acc cag cag att gtt ccg ttc ata cgg agc ctt	404
58	Asn Leu Ser Asp Gln Thr Gln Gln Ile Val Pro Phe Ile Arg Ser Leu	
59	5 10 15	
61	ctg atg cca aca acc gga ccg gcg tcc att ccg gac gac acc ctg gag	452
62	Leu Met Pro Thr Thr Gly Pro Ala Ser Ile Pro Asp Asp Thr Leu Glu	
63	20 25 30	
65	aag cac act ctc agg tca gag acc tcg acc tac aat ttg act gtg ggg	500
66	Lys His Thr Leu Arg Ser Glu Thr Ser Thr Tyr Asn Leu Thr Val Gly	

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70	Asp	Thr	Gly	Ser	Gly	Leu	Ile	Val
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73	att	gtg	ggt	gct	cac	tac	aca	ctg
74	Ile	Val	Gly	Ala	His	Tyr	Thr	Leu
75					70			75
77	gat	cag	atg	ctc	ctg	act	gcc	cag
78	Asp	Gln	Met	Leu	Leu	Thr	Ala	Gln
79					85			90
81	tgc	agg	cta	gtg	agt	cgg	agt	ctc
82	Cys	Arg	Leu	Val	Ser	Arg	Ser	Leu
83					100			105
85	ggt	ggc	ggt	tat	gca	cta	aac	ggc
86	Gly	Gly	Val	Tyr	Ala	Leu	Asn	Gly
87	115				120			125
89	gga	agc	ctg	agt	gaa	ctg	aca	gat
90	Gly	Ser	Leu	Ser	Glu	Leu	Thr	Asp
91					135			140
93	gca	aca	gcc	aac	atc	aac	gac	aaa
94	Ala	Thr	Ala	Asn	Ile	Asn	Asp	Lys
95					150			155
97	ggg	gtc	acc	gtc	ctc	agc	tta	ccc
98	Gly	Val	Thr	Val	Leu	Ser	Leu	Pro
99					165			170
101	agg	ctt	ggt	gac	ccc	att	ccc	gca
102	Arg	Leu	Gly	Asp	Pro	Ile	Pro	Ala
103					180			185
105	gcc	aca	tgt	gac	agc	agt	gac	agg
106	Ala	Thr	Cys	Asp	Ser	Ser	Asp	Arg
107	195				200			205
109	gcc	gat	gat	tac	caa	ttc	tca	tca
110	Ala	Asp	Asp	Tyr	Gln	Phe	Ser	Ser
111					215			220
113	atc	aca	ctg	ttc	tca	gcc	aac	att
114	Ile	Thr	Leu	Phe	Ser	Ala	Asn	Ile
115					230			235
117	ggg	gga	gag	ctc	gtg	ttt	cga	aca
118	Gly	Gly	Glu	Leu	Val	Phe	Arg	Thr
119					245			250
121	gcc	acc	atc	tac	ctc	ata	ggc	ttt
122	Ala	Thr	Ile	Tyr	Leu	Ile	Gly	Phe
123					260			265
125	gct	gtg	gcc	gca	aac	aat	ggg	ctg
126	Ala	Val	Ala	Ala	Asn	Asn	Gly	Leu
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129	cca	ttc	aat	ctt	gtg	att	cca	aca
130	Pro	Phe	Asn	Leu	Val	Ile	Pro	Thr
131					295			300

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133 tcc atc aaa ctg gag ata gtg acc tcc aaa agt ggt ggt cag gca ggg      1316
134 Ser Ile Lys Leu Glu Ile Val Thr Ser Lys Ser Gly Gly Gln Ala Gly
135          310          315          320
137 gat cag atg tca tgg tcg gca aga ggg agc cta gca gtg acg atc cat      1364
138 Asp Gln Met Ser Trp Ser Ala Arg Gly Ser Leu Ala Val Thr Ile His
139          325          330          335
141 ggt ggc aac tat cca ggg gcc ctc cgt ccc gtc acg cta gtg gcc tac      1412
142 Gly Gly Asn Tyr Pro Gly Ala Leu Arg Pro Val Thr Leu Val Ala Tyr
143          340          345          350
145 gaa aga gtg gca aca gga tcc gtc gtt acg gtc gct ggg gtg agc aac      1460
146 Glu Arg Val Ala Thr Gly Ser Val Val Thr Val Ala Gly Val Ser Asn
147 355          360          365          370
149 ttc gag ctg atc cca aat cct gaa cta gca aag aac ctg gtt aca gaa      1508
150 Phe Glu Leu Ile Pro Asn Pro Glu Leu Ala Lys Asn Leu Val Thr Glu
151          375          380          385
153 tac ggc cga ttt gac cca gga gcc atg aac tac aca aaa ttg ata ctg      1556
154 Tyr Gly Arg Phe Asp Pro Gly Ala Met Asn Tyr Thr Lys Leu Ile Leu
155          390          395          400
157 agt gag agg gac cgt ctt ggc atc aag acc gtc tgg cca aca agg gag      1604
158 Ser Glu Arg Asp Arg Leu Gly Ile Lys Thr Val Trp Pro Thr Arg Glu
159          405          410          415
161 tac act gac ttt cgt gaa tac ttc atg gag gtg gcc gac ctc aac tct      1652
162 Tyr Thr Asp Phe Arg Glu Tyr Phe Met Glu Val Ala Asp Leu Asn Ser
163          420          425          430
165 ccc ctg aag att gca gga gca ttc ggc ttc aaa gac ata atc cgg gcc      1700
166 Pro Leu Lys Ile Ala Gly Ala Phe Gly Phe Lys Asp Ile Ile Arg Ala
167 435          440          445          450
169 ata agg agg ata gct gtg taa gcttggtacc gcggctagct aagatccgct      1751
170 Ile Arg Arg Ile Ala Val
171          455
173 ctaaccgaaa aggaaggagt tagacaacct gaagtctagg tccctattta tttttttata      1811
175 gttatgttag tattaagaac gttatttata tttcaaattt ttcttttttt tctgtacaga      1871
177 cgcgtgtacg catgtaacat tatactgaaa accttgcttg agaagggtttt gggacgctcg      1931
179 aagatccagc tggcgtaata gcgaagaggc ccgcaccgat cgcccttccc aacagttgcg      1991
181 cagcctgaat ggcgaatgga cgcgcctgt agcggcgcat taagecgggc ggggtgtggtg      2051
183 gttacgcgca gcgtgaccgc tacacttgcc agcgccttag cgcccgctcc ttctgctttc      2111
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189 gatgggtcac gtagtgggcc atcgccctga tagacgggtt ttcgcccttt gacgttggag      2291
191 tccacgttct ttaatagtgg actcttggtc caaactggaa caacactcaa ccctatctcg      2351
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199 tataattaaa ttgaagctct aatttgtgag ttagtataac atgcatttac ttataataca      2591
201 gtttttttagt tttgctggcc gcactctctc aaatatgctt ccagcctgc ttttctgtaa      2651
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207 cccttgctat ctaaaccac accgggtgtc ataatcaacc aatcgtaacc ttcatctctt      2831
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211 tcaacagtac ccttagtata ttctccagta gatagggagc ccttgcatga caattctgct 2951
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215 acaataacctg ggcccaccac accgtgtgca ttcgtaatgt ctgcccattc tgctattctg 3071
217 tatacacccg cagagtactg caatttgact gtattaccaa tgtcagcaaa ttttctgtct 3131
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221 atggaaaaat cagtcaagat atccacatgt gtttttagta aacaaatfff gggacctaat 3251
223 gcttcaacta actccagtaa ttccctgggtg gtacgaacat ccaatgaagc acacaagttt 3311
225 gtttgctttt cgtgcatgat attaaatagc ttggcagcaa caggactagg atgagtagca 3371
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231 atatatacca atctaagtct gtgtcccttc cttcgttctt ccttctgttc ggagattacc 3551
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313 tctagcttcc cggcaacaat taatagactg gatggaggcg gataaagttg caggaccact 6011
315 tctgcgctcg gcccttccgg ctggctggtt tattgctgat aaatctggag ccggtgagcg 6071
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371 tatacatatc catatctaatt cttacttata tgttgtggaa atgtaaagag cccattatc 7751
373 ttagcctaaa aaaaccttct ctttggaact ttcagtaata cgcttaactg ctcattgcta 7811
375 tattgaagta cggattagaa gccgccgagc gggtgacagc cctccgaagg aagactctcc 7871
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380 &lt;210&gt; SEQ ID NO: 2

381 &lt;211&gt; LENGTH: 35

382 &lt;212&gt; TYPE: DNA

383 &lt;213&gt; ORGANISM: Artificial

385 &lt;220&gt; FEATURE:

386 &lt;223&gt; OTHER INFORMATION: Oligo I, direct oligonucleotide primer used for generating

the

387 DNA fragment encoding pVP2-456 protein in combination with SEQ ID

388 NO: 3

390 &lt;400&gt; SEQUENCE: 2

391 gcgcagatct atgacaaacc tgtcagatca aaccc

35

394 &lt;210&gt; SEQ ID NO: 3

395 &lt;211&gt; LENGTH: 32

396 &lt;212&gt; TYPE: DNA

397 &lt;213&gt; ORGANISM: Artificial

RAW SEQUENCE LISTING ERROR SUMMARY

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Invalid <213> Response:

Use of "Artificial" only as "<213> Organism" response is incomplete,  
per 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.

Seq#:1,2,3,4,5,6,7,8,9,10,11

VERIFICATION SUMMARY

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